

Seeley Lab rsfMRI preprocessing instructions

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System Requirements:

Unix-based Operating System

SPM12: Update the first line of SeeleyPreprocess/Paths.txt to contain the full path of your SPM12 directory.

FSL 5.0.4 or earlier (Version 5.0.7 not yet supported) Make sure there is an environment variable set called FSLDIR that lists your FSL path. This is usually set up as part of the FSL install. Type `echo $FSLDIR` if it returns nothing then you need to add to it to your system profile.

MATLAB: R2014b preferred for optimal interface graphics. Versions as old as R2013a are supported.

Sun Grid Engine (if parallel processing is desired)

Directory Setup:

Each subject has a top-level directory that is typically named with subjectID and date but this is not a requirement. The script only looks for folder structure and files within the top-level directory.

To setup a subject, create the following structure:

<top_level_directory>/:

struc/:

strucraw/: Put only the raw 3D .nii structural T1 file in struc/strucraw/

rsfmri/:

rawfmri/: Put only the raw 3D .nii BOLD fMRI files in rsfmri/rawfmri/

To run:

Prior to launching the Toolbox:

- In Matlab, create a cell array variable that lists **<top_level_directory>/rsfmri/**

for all of your subjects, like so:

```
subjdir={' /data5/patientNIC/10886/10886_20110621/rsfmri'
```

```
'/data5/patientNIC/10886/10886_20120109/rsfmri'
```

```
'/data5/patientNIC/12162/12162_20110509/rsfmri'}';
```

(must be a $n \times 1$ columnar cell array)

- Save the variable into a .mat file (The variable name must be subjdir but the file name can be whatever you choose): `save('subjdir_3_subjects.mat','subjdir')`

- Add the SeeleyPreprocess directory to your Matlab path
- Update the first line of SeeleyPreprocess/Paths.txt to contain the full path of your SPM12 directory.

Launching the Toolbox and running your jobs:

- Launch the Seeley Preprocessing Toolbox by running the command: 'Preprocess' in the matlab terminal.
- When prompted select the .mat file with your subjid variable.
- CHECK PARAMETERS: Review default parameters listed under "Pipeline Specifications" if your basic parameters differ or you would like to run a different configuration, click on "View & Edit Default Parameters"

It is important to check the basic parameters and customize them for your scanner/protocol characteristics. These include TR, Number of TRs and Slice Order. If you used an ascending or descending acquisition for your rsfMRI images, make sure you disable "Interleave Correct" under the 'Advanced Scanner Parameters' section.

- SCAN DIRECTORIES: When the "Pipeline Specifications" panel displays your desired configuration hit the "Scan Subject Directories" button. This will go into each of your subject's directories and will determine if the correct number of functional and structural files exist, corresponding to the user defined number of TRs and rsfMRI/Structural image prefixes.

After scanning completes, if the number listed under "Subjects ready to preprocess" does not match your number of subjects, check the failed subject listings by clicking the buttons next to each fail category and check the listed subject's directories to make sure they have the correct number of scans and the correct file prefixes.

- RUN: When the "Subjects ready to preprocess" count matches the count of your subject list, the last step before hitting run is to specify the processing type:

Parallel Processing- requires Sun Grid Engine to be installed, configured and "qsub" must be on the path. Matlab will pass to whatever queues are available to qsub. Each subject will be run on its own display-free instance of matlab in the background. Checking for Errors: Logs are saved to the subjects log directory in interfMRI_<output suffix> as text files that begin with e (errors) and o (stdout).

Serial Processing- Runs all subjects within the current matlab session, one at a time. Checking for Errors: If a subject in the list fails, the next

subject will begin processing and an error log will be saved to the failed subject's `interfmri_<output suffix>/log` directory named `PreprocError.mat`

Hit Run and refer to the command window in matlab for progress on job submission to SGE (if parallel) or progress on running each subject (if serial).

- CHECKING PROCESSING COMPLETION: See the Post-Processing Directory Organization below. A subject that completes successfully will have output images in the `processedfmri_<analysis_suffix>/images/` folder. These images are used as input to the first level analyses.

Post-Processing Directory Organization:

Each subject's data will be organized in the following fashion after preprocessing:

<top_level_directory>/:

struc/:

strucraw/: contains raw structural T1 .nii file

strucprocessed_<analysis_suffix>: contains processed T1 .nii files including skull stripped image (_brain) used for coregistration

rsfmri/:

rawfmri/: contains all raw 3D .nii BOLD fMRI files

***interfmri_<analysis_suffix>/:** where all intermediate files between raw and processed data are

***images/:** contains all 3D .nii fMRI files from intermediate stages of preprocessing

***melodic.ica/:** melodic ICA directory

motion_corr: motion correction file directory

motion_report.png: image file used to check fMRI

motion. Main values to check are "Max trans" (< 3 mm), "max rot" (< 3 degrees), "# spikes" (~ < 10% of total number of volumes)

***log/:** stores SPM job files and the subject-tailored

rsfmri_preprocess_MASTER.m script

example_func2standard.png: image file used to check fMRI normalization quality

***processedfmri_<analysis_suffix>/:**

***images/:** contains all 3D .nii fMRI files after all preprocessing is done

***Folders created by Preprocessing**